

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,541

DATE: 01/15/2002

TIME: 13:04:25

Input Set : A:\09914541.app

Output Set: N:\CRF3\01152002\I914541.raw

**ENTERED**

3 <110> APPLICANT: THE UNIVERSITY OF TENNESSEE RESEARCH CORPORATION  
4 BECKER, JEFFREY M.  
5 HAUSER, MELINDA  
6 DONHARDT, AMY  
7 BARNES, DAVID  
9 <120> TITLE OF INVENTION: EUKARYOTIC PEPTIDE UPTAKE SYSTEM FOR TRANSPORTING  
10 ENKEPHALINS  
12 <130> FILE REFERENCE: 1046-PCT-00  
14 <140> CURRENT APPLICATION NUMBER: 09/914541  
15 <141> CURRENT FILING DATE: 2001-08-29  
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/05158  
18 <151> PRIOR FILING DATE: 2000-03-01  
20 <150> PRIOR APPLICATION NUMBER: 60/122,312  
21 <151> PRIOR FILING DATE: 1999-03-01  
23 <160> NUMBER OF SEQ ID NOS: 26  
25 <170> SOFTWARE: PatentIn Ver. 2.1  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 2400  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Saccharomyces cerevisiae  
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35 gacgaggacg tcaataatct cactgcgact actgatgagg aggaccgcga tccggaaagc 180  
36 caaaaattcg acaggcattc catacaggag gaaggtctcg tttggaaggg cgaccctaca 240  
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38 accatccgcc tcaaccactg gagaacgtgg ttcttgacca cgggtgttgt ggtagttttc 360  
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40 gcacaagtgt tttgctaccc aattggtagg atactggctc tcttgcccga ctggaagtgt 480  
41 tctaaagtgc catttttcga tttaaaccgc ggccatttta ccaaaaagga acacgccgtg 540  
42 gtcacaattg ccgtggcgct tacttctctt actgcatacg ctatgtacat tttgaacgcc 600  
43 caggggaagct tttacaacat gaaacttaat gtcggatata agttcttggt ggtttgga 660  
44 tctcaaatga ttggttatgg tgctgcaggt cttaccagaa gatgggtcgt caaccctgca 720  
45 agctctatct ggcctcagac tttaatctca gtgtccttgt ttgattcggt gcactcgaga 780  
46 aaagtgtaaa agacagtcgc aaatggttgg acgatgcccc gttacagggt cttcttaatc 840  
47 gtccttatcg gatcggttat ctggtattgg gtacctggat tcctctttac cggctctgtc 900  
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57 cccgattggg ggtattttact tttgcagatt gtcattgatc gtttaggatt tgtagcagtg 1500  
58 tgctgtttcg atactaagtt cccagcttgg gcatttggtt ttgcaatatt aatttccctt 1560

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59 gtaaatttca tcccgaagg tatcttggaa gcaatgacta accaacacgt aggtttgaat 1620
60 attatcacag aattgatctg cggttatatg ctgcctttaa gaccaatggc aaacttatta 1680
61 ttcaagctat acggatttat tgatcatgaga caaggcttga atttgagtag agatttgaaa 1740
62 ttagccatgt acatgaagggt ttcccctcgt ttgatctttg ccgttcaaat ctatgccact 1800
63 atcatatcag gcatgggttaa cgttgggtgtc caggaatgga tgatgcataa tatcgatggc 1860
64 ttatgtacca ccgatcaacc aaatggcttc acttgtgcta atggtcgcac ggttttcaat 1920
65 gcttccatta totggtcttt gccaaagtat cttttctcat cagggcgcat ttataatccg 1980
66 ctgatgtggt tcttcttgat tggtttgcta tcccactag ccgtttatgc tgttcaatgg 2040
67 aaattcccta aatttaaatt tgctaagcac attcactctc ctgtattttt cacaggccca 2100
68 ggtaatatcc caccaagcac acctataaac tactcattat tttttgcaat gtcattctgc 2160
69 ctaaacttga taagaaaaag atggagagct tggttcaata agtacaattt cgtcatgggg 2220
70 gccggtgttg aagcaggtgt ggcaatctcc gtcgtcatca tcttcttggtg tgtacagtac 2280
71 ccaggtggtg agctcagctg gtgggggaaac aacgttttga aaagaacgta tgataatgat 2340
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75 &lt;210&gt; SEQ ID NO: 2

76 &lt;211&gt; LENGTH: 799

77 &lt;212&gt; TYPE: PRT

78 <213> ORGANISM: *Saccharomyces cerevisiae*

80 &lt;400&gt; SEQUENCE: 2

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85           20           25           30
87 Lys Asp Ala Phe Val Lys Asn Ile Asp Glu Asp Val Asn Asn Leu Thr
88           35           40           45
90 Ala Thr Thr Asp Glu Glu Asp Arg Asp Pro Glu Ser Gln Lys Phe Asp
91           50           55           60
93 Arg His Ser Ile Gln Glu Glu Gly Leu Val Trp Lys Gly Asp Pro Thr
94   65           70           75           80
96 Tyr Leu Pro Asn Ser Pro Tyr Pro Glu Val Arg Ser Ala Val Ser Ile
97           85           90           95
99 Glu Asp Asp Pro Thr Ile Arg Leu Asn His Trp Arg Thr Trp Phe Leu
100          100          105          110
102 Thr Thr Val Phe Val Val Val Phe Ala Gly Val Asn Gln Phe Phe Ser
103          115          120          125
105 Leu Arg Tyr Pro Ser Leu Glu Ile Asn Phe Leu Val Ala Gln Val Val
106          130          135          140
108 Cys Tyr Pro Ile Gly Arg Ile Leu Ala Leu Leu Pro Asp Trp Lys Cys
109 145           150           155           160
111 Ser Lys Val Pro Phe Phe Asp Leu Asn Pro Gly Pro Phe Thr Lys Lys
112          165          170          175
114 Glu His Ala Val Val Thr Ile Ala Val Ala Leu Thr Ser Ser Thr Ala
115          180          185          190
117 Tyr Ala Met Tyr Ile Leu Asn Ala Gln Gly Ser Phe Tyr Asn Met Lys
118          195          200          205
120 Leu Asn Val Gly Tyr Gln Phe Leu Leu Val Trp Thr Ser Gln Met Ile
121          210          215          220
123 Gly Tyr Gly Ala Ala Gly Leu Thr Arg Arg Trp Val Val Asn Pro Ala
124 225          230          235          240

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126 Ser Ser Ile Trp Pro Gln Thr Leu Ile Ser Val Ser Leu Phe Asp Ser
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129 Leu His Ser Arg Lys Val Glu Lys Thr Val Ala Asn Gly Trp Thr Met
130          260          265          270
132 Pro Arg Tyr Arg Phe Phe Leu Ile Val Leu Ile Gly Ser Phe Ile Trp
133          275          280          285
135 Tyr Trp Val Pro Gly Phe Leu Phe Thr Gly Leu Ser Tyr Phe Asn Val
136          290          295          300
138 Ile Leu Trp Gly Ser Lys Thr Arg His Asn Phe Ile Ala Asn Thr Ile
139 305          310          315          320
141 Phe Gly Thr Gln Ser Gly Leu Gly Ala Leu Pro Ile Thr Phe Asp Tyr
142          325          330          335
144 Thr Gln Val Ser Gln Ala Met Ser Gly Ser Val Phe Ala Thr Pro Phe
145          340          345          350
147 Tyr Val Ser Ala Asn Thr Tyr Ala Ser Val Leu Ile Phe Phe Val Ile
148          355          360          365
150 Val Leu Pro Cys Leu Tyr Phe Thr Asn Thr Trp Tyr Ala Lys Tyr Met
151          370          375          380
153 Pro Val Ile Ser Gly Ser Thr Tyr Asp Asn Thr Gln Asn Lys Tyr Asn
154 385          390          395          400
156 Val Thr Lys Ile Leu Asn Glu Asp Tyr Ser Ile Asn Leu Glu Lys Tyr
157          405          410          415
159 Lys Glu Tyr Ser Pro Val Phe Val Pro Phe Ser Tyr Leu Leu Ser Tyr
160          420          425          430
162 Ala Leu Asn Phe Ala Ala Val Ile Ala Val Phe Val His Cys Ile Leu
163          435          440          445
165 Tyr His Gly Lys Asp Ile Val Ala Lys Phe Lys Asp Arg Lys Asn Gly
166          450          455          460
168 Gly Thr Asp Ile His Met Arg Ile Tyr Ser Lys Asn Tyr Lys Asp Cys
169 465          470          475          480
171 Pro Asp Trp Trp Tyr Leu Leu Leu Gln Ile Val Met Ile Gly Leu Gly
172          485          490          495
174 Phe Val Ala Val Cys Cys Phe Asp Thr Lys Phe Pro Ala Trp Ala Phe
175          500          505          510
177 Val Ile Ala Ile Leu Ile Ser Leu Val Asn Phe Ile Pro Gln Gly Ile
178          515          520          525
180 Leu Glu Ala Met Thr Asn Gln His Val Gly Leu Asn Ile Ile Thr Glu
181          530          535          540
183 Leu Ile Cys Gly Tyr Met Leu Pro Leu Arg Pro Met Ala Asn Leu Leu
184 545          550          555          560
186 Phe Lys Leu Tyr Gly Phe Ile Val Met Arg Gln Gly Leu Asn Leu Ser
187          565          570          575
189 Arg Asp Leu Lys Leu Ala Met Tyr Met Lys Val Ser Pro Arg Leu Ile
190          580          585          590
192 Phe Ala Val Gln Ile Tyr Ala Thr Ile Ile Ser Gly Met Val Asn Val
193          595          600          605
195 Gly Val Gln Glu Trp Met Met His Asn Ile Asp Gly Leu Cys Thr Thr
196          610          615          620
198 Asp Gln Pro Asn Gly Phe Thr Cys Ala Asn Gly Arg Thr Val Phe Asn

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199 625          630          635          640
201 Ala Ser Ile Ile Trp Ser Leu Pro Lys Tyr Leu Phe Ser Ser Gly Arg
202          645          650          655
204 Ile Tyr Asn Pro Leu Met Trp Phe Phe Leu Ile Gly Leu Leu Phe Pro
205          660          665          670
207 Leu Ala Val Tyr Ala Val Gln Trp Lys Phe Pro Lys Phe Lys Phe Ala
208          675          680          685
210 Lys His Ile His Thr Pro Val Phe Phe Thr Gly Pro Gly Asn Ile Pro
211          690          695          700
213 Pro Ser Thr Pro Tyr Asn Tyr Ser Leu Phe Phe Ala Met Ser Phe Cys
214 705          710          715          720
216 Leu Asn Leu Ile Arg Lys Arg Trp Arg Ala Trp Phe Asn Lys Tyr Asn
217          725          730          735
219 Phe Val Met Gly Ala Gly Val Glu Ala Gly Val Ala Ile Ser Val Val
220          740          745          750
222 Ile Ile Phe Leu Cys Val Gln Tyr Pro Gly Gly Lys Leu Ser Trp Trp
223          755          760          765
225 Gly Asn Asn Val Trp Lys Arg Thr Tyr Asp Asn Asp Tyr Lys Lys Phe
226          770          775          780
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229 785          790          795
232 <210> SEQ ID NO: 3
233 <211> LENGTH: 753
234 <212> TYPE: PRT
235 <213> ORGANISM: Arabidopsis thaliana
237 <400> SEQUENCE: 3
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239 1 5 10 15
241 Ser Lys Ile Val Ile Ala Asp Glu Glu Glu Glu Asp Glu Asn Asp Ser
242 20 25 30
244 Pro Ile Glu Glu Val Arg Leu Thr Val Pro Ile Thr Asp Asp Pro Ser
245 35 40 45
247 Leu Pro Val Leu Thr Phe Arg Thr Trp Phe Leu Gly Met Val Ser Cys
248 50 55 60
250 Val Val Leu Ala Phe Val Asn Asn Phe Phe Gly Tyr Arg Ser Asn Pro
251 65 70 75 80
253 Leu Thr Val Ser Ser Val Val Ala Gln Ile Ile Thr Leu Pro Leu Gly
254 85 90 95
256 Lys Leu Met Ala Thr Thr Leu Pro Thr Thr Lys Leu Arg Leu Pro Gly
257 100 105 110
259 Thr Asn Trp Ser Cys Ser Leu Asn Pro Gly Pro Phe Asn Met Lys Glu
260 115 120 125
262 His Val Leu Ile Thr Ile Phe Ala Asn Thr Gly Ala Gly Gly Ala Tyr
263 130 135 140
265 Ala Thr Ser Ile Leu Thr Ile Val Lys Ala Phe Tyr His Arg Asn Leu
266 145 150 155 160
268 Asn Pro Ala Ala Ala Met Leu Leu Val Gln Thr Thr Gln Leu Leu Gly
269 165 170 175
271 Tyr Gly Trp Ala Gly Met Phe Arg Lys Tyr Leu Val Asp Ser Pro Tyr

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272          180          185          190
274 Met Trp Trp Pro Ala Asn Leu Val Gln Val Ser Leu Phe Arg Ala Leu
275          195          200          205
277 His Glu Lys Glu Glu Lys Arg Glu Gly Lys Gln Thr Lys Leu Arg Phe
278          210          215          220
280 Phe Leu Ile Val Phe Phe Leu Ser Phe Thr Tyr Tyr Ile Val Pro Gly
281 225          230          235          240
283 Tyr Leu Phe Pro Ser Ile Ser Tyr Leu Ser Phe Val Cys Trp Ile Trp
284          245          250          255
286 Thr Arg Ser Val Thr Ala Gln Gln Ile Gly Ser Gly Leu His Gly Leu
287          260          265          270
289 Gly Ile Gly Ser Phe Gly Leu Asp Trp Ser Thr Val Ala Gly Phe Leu
290          275          280          285
292 Gly Ser Pro Leu Ala Val Pro Phe Phe Ala Ile Ala Asn Ser Phe Gly
293          290          295          300
295 Gly Phe Ile Ile Phe Phe Tyr Ile Ile Leu Pro Ile Phe Tyr Trp Ser
296 305          310          315          320
298 Asn Ala Tyr Glu Ala Lys Lys Phe Pro Phe Tyr Thr Ser His Pro Phe
299          325          330          335
301 Asp His Thr Gly Gln Arg Tyr Asn Thr Thr Arg Ile Leu Asn Gln Lys
302          340          345          350
304 Thr Phe Asn Ile Asp Leu Pro Ala Tyr Glu Ser Tyr Ser Lys Leu Tyr
305          355          360          365
307 Leu Ser Ile Leu Phe Ala Leu Ile Tyr Gly Leu Ser Phe Gly Thr Leu
308          370          375          380
310 Thr Ala Thr Ile Ser His Val Ala Leu Phe Asp Gly Lys Phe Ile Trp
311 385          390          395          400
313 Glu Leu Trp Lys Lys Ala Thr Leu Thr Thr Lys Asp Lys Phe Gly Asp
314          405          410          415
316 Val His Thr Arg Leu Met Lys Lys Asn Tyr Lys Glu Val Pro Gln Trp
317          420          425          430
319 Trp Phe Val Ala Val Leu Ala Ala Ser Phe Val Leu Ala Leu Tyr Ala
320          435          440          445
322 Cys Glu Gly Phe Gly Lys Gln Leu Gln Leu Pro Trp Trp Gly Leu Leu
323          450          455          460
325 Leu Ala Cys Ala Ile Ala Phe Thr Phe Thr Leu Pro Ile Gly Val Ile
326 465          470          475          480
328 Leu Ala Thr Thr Asn Gln Arg Met Gly Leu Asn Val Ile Ser Glu Leu
329          485          490          495
331 Ile Ile Gly Phe Leu Tyr Pro Gly Lys Pro Leu Ala Asn Val Ala Phe
332          500          505          510
334 Lys Thr Tyr Gly Ser Val Ser Ile Ala Gln Ala Leu Tyr Phe Val Gly
335          515          520          525
337 Asp Phe Lys Leu Gly His Tyr Met Lys Ile Pro Pro Arg Ser Met Phe
338          530          535          540
340 Ile Val Gln Leu Val Ala Thr Ile Val Ala Ser Thr Val Ser Phe Gly
341 545          550          555          560
343 Thr Thr Trp Trp Leu Ser Ser Val Glu Asn Ile Cys Asn Thr Asp
344          565          570          575

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/914,541

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Input Set : A:\09914541.app

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L:2570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24

L:2599 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26

L:2599 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26

L:2599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26